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January 25, 2000

Ms. Allison B. Rumsey
U.S. Deparument of Justice
Office of Assistant Attorney General
950 Pennsylvania Ave., N W.
Washington, D.C. 20530-0001

VIA FAX AND MAIL
(202) 514-0557

Re: Bonnichsen et.al. v. U.S.
Civil No. 96-1481-JE

Dear Allison:

Enclosed is a copy of an affidavit from Dr. Theodore G. Schurr concerning DNA testing of the Kennewick Skeleton. Because of its length, the two Appendixes (and their related tables and figures) have not been included with the faxed copy of this letter. They will, however, be included with the mailed copy.

Another affidavit on this subject by Dr. David Glenn Smith of UC Davis is currently being prepared, and will be sent to you when it has been completed. I anticipate that I will be able to send it to you within the next week (if not sooner).

Please forward these materials to your clients for their consideration as part of their proceedings relating to the Kennewick skeleton.

Very truly yours,

Alan L. Schneider

Alan L. Schneider

ALS/kfk
Enclosure
cc: P. Barran
R. Donaldson
T. Schurr
D. Smith
C. Hawkinson
Clients

DOI 06700

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Attorneys for Plaintiff

IN THE UNITED STATES DISTRICT COURT

FOR THE DISTRICT OF OREGON

ROBSON BONNICHSEN, et.al., Plaintiffs, v. UNITED STATES OF AMERICA, DEPARTMENT OF THE ARMY, et.al., Defendants.	USDC No. CV 96-1481 JE AFFIDAVIT OF THEODORE G. SCHURR

STATE OF TEXAS)
)ss.
County of Bexar)

I, Theodore G. Schurr being first duly sworn, do depose and state as follows:

1. I am a Post-Doctoral Scientist in the Department of Genetics at the Southwest Foundation for Biomedical Research ("SFBR"), San Antonio, Texas. My area of expertise is the study and analysis of mitochondrial DNA ("mtDNA") and Y chromosome variation in modern human populations, in particular,

the indigenous populations of Siberia and the Americas. I make this affidavit in support of the plaintiffs' motion to gain access to the Kennewick Man skeleton for the purpose of undertaking the scientific studies and analyses described in that motion. Specifically, this affidavit will address the following issues: (a) the importance and relevance of performing genetic tests on the skeleton; (b) how such tests should be performed and the results analyzed.

2. My professional qualifications are as follows: I hold an M.A. and Ph.D. in Anthropology which I received from Emory University in 1996 and 1998, respectively, and a Bachelor's degree in Zoology which I received from the University of Georgia in 1983. Between earning my Bachelor's degree and completing the Ph.D., I worked for three years as a Research Technician in the Department of Genetics at the University of Georgia, where I conducted research on genes involved in photosynthesis, and then another five years as a Research Technician in the Department of Genetics and Molecular Medicine at Emory University, where I conducted research into both clinical and anthropological genetics of human populations. After graduating from Emory University, I worked briefly as a Post-Doctoral Fellow in the Center for Molecular Medicine at Emory University. I then took my current Post-Doctoral Scientist position at SFBR. At present, I am participating in a long-term National Institute of Health project called the Strong Heart Family Study which involves the mapping and identification of genes that contribute to cardiovascular disease risk in Native Americans.

3. For the past ten years, the main focus of my work has been investigating the peopling of the Americas from a biogenetic perspective. This work has involved the analysis of mtDNA variation in approximately 1000 native Siberian and approximately 600 Native American individuals from 50 different populations, and the analysis of Y-chromosome variation in the majority of those individuals. While most of my research has taken place in the laboratory, I have also conducted field research with Russian colleagues in northeastern Siberia to gain a better understanding of population histories in that region. In addition to these studies, I have been involved in numerous other molecular genetic analyses of African,

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Asian, Aboriginal Australian, and European/Caucasian populations, and these have collectively given me a broad understanding of population genetic variation in human groups. Based on these studies, I have co-authorized nearly 50 scientific articles and papers. These include articles published in scientific journals, review articles, papers presented at scientific conferences, and chapters for books on anthropological issues.

4. Genetic research conducted by myself, my colleagues at Emory University, and other scientists over the past decade has provided a number of seminal insights into the peopling of the New World. DNA analyses of modern populations and prehistoric skeletal remains have provided important new information about the timing of human colonization of the Americas, the number of migrations that reached the New World, and the potential source area(s) from which the early New World colonizing population(s) originated. Overall, the data obtained from DNA research imply that the colonization of the Americas was a more complex process than suggested by earlier models, one that has a greater time depth and involves more colonizing groups than previously thought. A general overview of these insights is provided below. More details can be found in Appendixes A and B attached to this affidavit. Appendix A provides technical details concerning the properties of the two genetic systems that have commonly been used for population affiliation studies, the mtDNA and the Y-chromosome. Appendix B describes the genetic characteristics of modern New World native populations. These characteristics provide critical baseline information that are needed for any efforts to determine the population affinities of the Kennewick skeleton.

5. For many years, the ruling "paradigm" in scientific thought concerning the peopling of the Americas was the Clovis First Model. According to this model, the New World was first colonized by a small band of Ice Age big-game hunters who gained access to the interior of North America via an ice-free corridor in west-central Canada approximately 11,700 years before present ("YBP"). From the southern end of this ice-free corridor (somewhere in the vicinity of modern Montana), this small band of humans supposedly radiated outward so rapidly that, within less than 1,500 years, their descendants had reached the tip of South America. Modern genetic research has brought these postulates of the Clovis First Model into

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question.

A. The Clovis First Model postulates that the New World was colonized by people of Asian origin. DNA data have confirmed this postulate, at least for the most part. The majority of mtDNAs and Y-chromosomes of modern New World native populations contain genetic markers indicating that their ancestors originated in Asia. See Appendix B, Paragraphs 16, 17.

B. The Clovis First Model also postulates that the peopling of the New World is attributable to a single colonizing event. DNA studies do not support that postulate. The most common mtDNA lineages found in modern New World native populations belong to haplogroups A, B, C and D. See Appendix B, Paragraph 2. Two of these haplogroups (A and B) appear to have originated in southeast Siberia or Mongolia, although haplogroup B seems to have a strong East Asian distribution. Appendix B, Paragraph 16A. Haplogroups C and D, on the other hand, may have had multiple source areas in Asia, including southeastern Siberia and the Amur River region. Appendix B, Paragraph 16B. In addition, a mtDNA lineage found in varying frequencies in modern New World populations, haplogroup X, appears to be distantly related to a similar haplogroup found in European populations. Appendix B, Paragraph 13. Although the original source area for haplogroup X has yet to be determined, it does not appear to be east Asia. Such data appear to indicate that the colonizers of the New World did not originate in a single limited region of the Asian landmass. If they did not, then the case for a single colonizing event becomes less plausible.

C. Another postulate of the Clovis First Model is that the original colonizers of the New World consisted of a small band that contained only a few hundred members (or at most a few thousand). One corollary of this postulate is that all modern New World native peoples would share the same degree of biological relationship to one another and to the original colonizing group. Under this view, the genetic and morphological differences between modern native populations would merely be a reflection of the different historical events (e.g., genetic drift, founder effects, natural selection) they experienced after separation in

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the New World. However, the DNA data discussed in Paragraph B above does not support these conclusions. If the New World was in fact colonized by multiple groups at different times, then the differences between modern native peoples reflect different genetic inputs as well as their particular historic experiences. As a result, some modern native groups will have a closer, and others a more remote, biological connection to specific early New World populations. For some groups, the connection may be almost nonexistent, or indirect at best.

D. Another postulate of the Clovis First Model is that the New World was not colonized until approximately 11,700 YBP. This postulate is inconsistent with dates obtained through statistical analyses of DNA data. Various researchers have used DNA data to estimate the timing of New World colonization by calculating how long ago the genetic lineages found in modern Native Americans split from their progenitors in Asia. The divergence times calculated for the different genetic lineages range on average from 38,139 YBP to 23,097 YBP, depending on the data and methods used. The most probable conclusion is that mtDNA haplogroups A-D arrived in the New World well before 18,000 YBP, with haplogroup X arriving either before or after this time. See Appendix B, Paragraphs 11, 14.

6. It is my understanding that answers are being sought to two questions concerning the Kennewick Man skeleton: (a) is it related to present-day U.S. Native Americans; (b) is it affiliated to any of the five tribes that have claimed it? By necessity, any attempt to resolve these questions must rely primarily on biological and genetic analyses of the skeleton. There are no cultural artifacts associated with the skeleton other than the projectile point fragment lodged in its hip. Even if this fragment can be identified as belonging to a particular lithic tradition, there is no objective way to determine whether it was manufactured by Kennewick Man's tribe or by some other, possibly hostile, group of people. Furthermore, utilitarian artifacts such as projectile points may not be the best indicators of group identity because unrelated populations may use similar tools as a result of cultural borrowing or trade. Likewise, arguments based on linguistic criteria will be essentially unhelpful. Since dead men can't speak, there is no way to know what

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language Kennewick Man spoke during his lifetime. Thus, without symbolically interpretable artifacts or evidence of linguistic affiliation, one can only speculate as to whether Kennewick Man's cultural conception of the world, mythology, clan structure and other symbolic elements used to determine his social and cultural identity, were the same as those of any modern Native American tribe.

7. The only things that can definitely be known about Kennewick Man are what his skeleton can tell us. In fact, much can be learned from skeletal and dental studies (i.e., metric measurements and discrete traits observations). These lines of evidence can provide important insights into Kennewick Man's biological affinities to different modern and prehistoric human populations. However, they provide only part of the needed information. Anatomical features such as teeth and cranial features indirectly reflect the underlying genetic relationships between populations and individuals because the genes influencing those traits are not known. In contrast, DNA analyses can measure those relationships directly. Among other things, DNA data can determine whether Kennewick Man is genetically similar to modern Native Americans, or whether he possesses genetic markers not typical of contemporary native populations. In addition, depending upon the specific markers that are found, DNA data may possibly be able to tell us whether Kennewick Man is genetically closer to one tribe (or group of tribes) than to others. Such data, together with skeletal and dental data, can provide an objective and rational basis for assessing this individual's population affinities.

8. If DNA testing of the skeleton is permitted, the testing protocol should be designed to obtain as much information as possible. In this regard, I recommend that, at a minimum, the following tests should be performed:

A. The mtDNA from the skeleton should be subjected to restriction fragment length polymorphism (or "RFLP") analysis. This method determines the extent to which the mtDNAs of different individuals are the same or dissimilar at certain discrete locations (called "recognition sites") in their sequences of nucleotide bases. See Appendix A, Paragraph 3. All of the RFLPs present in a human mtDNA defines its

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"haplotype." Haplotypes that share a specific set of RFLPs are said to belong to a "haplogroup" or, alternatively, a "mtDNA lineage", because they are genealogically related. See Appendix A, Paragraph 7. Of these RFLPs, only a small subset of them identify specific haplogroups, and, hence, constitute the diagnostic genetic markers for these mtDNA lineages. To date, the only haplogroups found in modern New World populations that are thought to predate European contact are haplogroups A, B, C, D and X. See Appendix B, Paragraphs 4 and 14. Consequently, Kennewick Man's mtDNA should be screened for the RFLPs that define these haplogroups. If none of them are detected, then the skeleton should be tested for RFLPs which define other known Asian haplogroups.

B. DNA testing of the skeleton should also include the direct sequencing of at least the first hypervariable segment ("HVS-I") of the mtDNA control region ("CR"). In contrast to RFLP analysis which scans the genome for isolated sequence changes at selected recognition sites, CR sequencing provides a nucleotide-by-nucleotide decoding of a sizeable piece of the mtDNA. See Appendix A, Paragraph 6. Variation in CR nucleotide sequences often provides information about lineal identity of mtDNAs, and can be used to distinguish otherwise identical RFLP haplotypes from each other. As a result, they increase our ability to reconstruct the genetic histories and relationships of different mtDNA lineages (and of the individuals who share those lineages).

C. DNA testing of the skeleton should also include an attempt to define its Y-chromosome haplogroup, or paternal lineage. The Y chromosome is the male counterpart of mtDNA. Whereas mtDNA is inherited from an individual's mother, Y chromosomes are transmitted only through the male members of a family tree (females possess only X chromosomes). To date, two Asian paternal lineages that are thought to predate the era of European contact comprise the vast majority of Y-chromosomes found in modern New World native populations. See Appendix B, Paragraph 17. Tests should be conducted on the Kennewick skeleton for these two haplogroups. If they are not found, tests for other Y-chromosome haplogroups should be performed.

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9. Analyzing ancient DNA is more complicated than analyzing modern DNA. Ancient DNA is usually degraded (i.e., broken into many small segments) because of normal processes of deterioration in the skeleton, and sometimes because of post-mortem environmental conditions. As a result, extraction and PCR amplification (replication) of these fragments can be difficult. In addition, special care must be taken during the analysis to avoid contamination by DNA from modern sources. Consequently, the testing of the Kennewick skeleton should be conducted by scientists experienced in the unique challenges presented by ancient DNA research. To ensure the reliability of the data obtained, samples from the skeleton should be tested by at least two different laboratories, much as was done with the recently analyzed Neandertal skeleton.

10. Equally critical is the process used for the analysis of the test results. Some of the relevant considerations in this regard include the following:

A. The evaluation and interpretation of the test results should be conducted by scientists who are familiar with both ancient human DNA research and First Americans issues. Not all DNA researchers have the necessary background in these areas. In addition, since individual scientists can differ in their interpretations of data, an effort should be made to obtain as many different viewpoints as possible.

B. The test results should be compared to all relevant published DNA data. Such data should include mtDNA and Y chromosome data for both modern and prehistoric New World native populations, and for relevant groups in Asia and elsewhere in the world. In addition, analyses should be requested from researchers who have databases of unpublished DNA information. For example, I have unpublished DNA data from Siberian and other Asian populations that could be helpful in interpreting any test results from the Kennewick skeleton. Other researchers interested in First Americans issues may also have relevant unpublished information.

C. Since one purpose of this process is to determine if the skeleton can be affiliated to any of the tribes that have claimed it, a special effort should be made to obtain comparative data specific to those

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tribes. Without such data, any decision upholding their claims would lack an adequate factual foundation. Accordingly, the claiming tribes should be asked if their members will provide blood or buccal (cheek) cell samples for DNA testing. If they will not, then it may be possible to obtain DNA samples for these tribes from skeletal or other biological materials held in archaeological collections.

11. It cannot be predicted in advance what kind of DNA data will be obtained from the Kennewick skeleton if testing is permitted, or what conclusions will be appropriate to draw from those data. There are many possibilities. For example, tribal claims would be enhanced if the skeleton is found to contain one of the genetic lineages (such as mtDNA haplogroups A, B, C, D or X) that are known to predate European contact. All other things being equal, their presence in the skeleton would be consistent with the conclusion that Kennewick Man represents a population that contributed to the ancestry of modern U.S. Native Americans. However, they would not be conclusive proof of ancestry because these haplogroups are not unique to U.S. native populations. On the other hand, it is possible that DNA testing could discover one or more genetic markers that are unique to this skeleton and one of the claiming tribes. If this were the case, then the inference of an ancestral-descendant relationship would be difficult to dispute. This is why all of the abovementioned genetic data should be obtained, as they are needed to delineate between the genetic markers present in Asian/Eurasian DNAs from those appearing in modern New World native populations. Conversely, tribal claims would be weakened if the skeleton were found to contain genetic markers that are not known to be characteristic of modern New World native populations. Once again, however, such data would not be absolutely conclusive.

12. In any of these possible scenarios, the final conclusions about the skeleton's population affinities should be made in light of all of the information that can be obtained from it, whether it be genetic, osteological, dental, or biochemical. Should all such information be entirely consistent in pointing to the same conclusion, then our overall interpretation will become more robust. Conversely, if the data obtained from different studies appear to be inconsistent with one another, then each line of evidence must

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be carefully reviewed and assessed to determine what it is telling us. In some cases, it may be difficult to reconcile the different data sets and reach an unambiguous conclusion. Such a situation would not necessarily mean that these data are inaccurate or irrelevant, but only that more data are required to make a more certain ascertainment of the skeleton's biological status.

13. While DNA data cannot be predicted to conclusively establish Kennewick Man's population affiliations, any decision concerning the skeleton's fate will be deficient if it does not take this line of evidence into account. DNA is the only source of information that directly assesses the underlying genetic relationships (or lack thereof) between and among populations. Only DNA analyses can directly establish the shared genetic characteristics of all human groups and the broad geneological links between populations within various geographic regions, as well as more localized genetic differences between different population subgroups. In situations of this kind, DNA is a line of evidence that cannot be reasonably disregarded.

14. On a broader level, DNA data from the Kennewick skeleton is important because of the contributions such information could make to our understanding of the processes that resulted in the peopling of the Americas. New statistical analyses of cranial and skeletal data from New World populations have begun to reveal anatomical differences between ancient Paleoamerican or "Paleoindian" human remains and those dating from the Archaic period forward to modern times. However, it is not completely clear what caused these differences. They could be attributable to the occurrence of multiple, temporally distinct migrations from different parts of Asia to the Americas. On the other hand, they could reflect the *in situ* biological differentiation of native populations because of geographic isolation from ancestral populations in Asia, and subsequent contact since that time between widely scattered populations in the Americas. In either case, data from studies of Paleoamerican remains are needed to clarify these questions since such remains represent the earliest known occupants of the New World.

15. The study of Paleoamerican remains will help scientists more accurately reconstruct the prehistory

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of the Americas. While molecular genetics has enlarged our understanding of the biological links between Asian and Native American peoples, this field has not provided answers to all of the questions concerning the origins and affinities of New World populations. Improvements in our understanding of the timing and processes of the colonization of the New World requires study of the geography and geology of Siberia and the Americas, the languages of modern Native American peoples, the cultural diversity of these populations, and the biological variation present within them. In other words, one must consider the totality of anthropological evidence pertaining to Native American origins to gain the most complete picture of the peopling of the New World, and this includes biological information available through the examination of Paleoamerican skeletons.

16. I have no personal stake in testing of the Kennewick Man skeleton, nor any prejudices about the ultimate outcome of this study, which I would evaluate fairly and impartially if given the opportunity. Moreover, I have nothing to gain from an erroneous or inaccurate determination of the biological affinities of this skeleton.

DATED this 21st day of January, 2000.

Theodore G. Schurr

SUBSCRIBED and SWORN to before me this 21st day of January, 2000.

Notary Public for BEXAR County
My Commission Expires: 1/4/02

LOUISE SKOW
Notary Public, State of Texas
My Commission Expires Jan. 4, 2002

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